

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Feder, John N.  
Bjorkman, Pamela J.  
Schatzman, Randall C.
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES  
AND IRON DEFICIENCY DISEASES
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pennie & Edmonds, LLP  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: NY  
(E) COUNTRY: USA  
(F) ZIP: 10036-2811
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: to be assigned  
(B) FILING DATE: June 12, 1998  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/876,010  
(B) FILING DATE: June 13, 1997
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Poissant, Brian M  
(B) REGISTRATION NUMBER: 28,462  
(C) REFERENCE/DOCKET NUMBER: 8907-0074-999
- (ix) TELECOMMUNICATION INFORMATION:  
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 276 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser  
1 5 10 15  
Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp

Asp	Gln	Leu	20	Phe	Val	Phe	Tyr	Asp	25	His	Glu	Ser	Arg	Arg	30	Val	Glu	Pro
		35						40						45				
Arg	Thr	Pro	Trp	Val	Ser	Ser	Arg	Ile	Ser	Ser	Gln	Met	Trp	Leu	Gln			
	50					55					60							
Leu	Ser	Gln	Ser	Leu	Lys	Gly	Trp	Asp	His	Met	Phe	Thr	Val	Asp	Phe			
65					70					75					80			
Trp	Thr	Ile	Met	Glu	Asn	His	Asn	His	Ser	Lys	Glu	Ser	His	Thr	Leu			
			85						90					95				
Gln	Val	Ile	Leu	Gly	Cys	Glu	Met	Gln	Glu	Asp	Asn	Ser	Thr	Glu	Gly			
			100					105					110					
Tyr	Trp	Lys	Tyr	Gly	Tyr	Asp	Gly	Gln	Asp	His	Leu	Glu	Phe	Cys	Pro			
		115					120						125					
Asp	Thr	Leu	Asp	Trp	Arg	Ala	Ala	Glu	Pro	Arg	Ala	Trp	Pro	Thr	Lys			
	130					135					140							
Leu	Glu	Trp	Glu	Arg	His	Lys	Ile	Arg	Ala	Arg	Gln	Asn	Arg	Ala	Tyr			
145					150					155					160			
Leu	Glu	Arg	Asp	Cys	Pro	Ala	Gln	Leu	Gln	Gln	Leu	Leu	Glu	Leu	Gly			
			165						170					175				
Arg	Gly	Val	Leu	Asp	Gln	Gln	Val	Pro	Pro	Leu	Val	Lys	Val	Thr	His			
		180						185					190					
His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr			
	195						200					205						
Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met			
	210					215					220							
Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	Gly	Asp	Gly			
225					230					235					240			
Thr	Tyr	Gln	Gly	Trp	Ile	Thr	Leu	Ala	Val	Pro	Pro	Gly	Glu	Glu	Gln			
			245						250					255				
Arg	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Gly	Leu	Asp	Gln	Pro	Leu	Ile			
		260						265					270					
Val	Ile	Trp	Glu															
		275																

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Arg	Leu	Leu	Arg	Ser	His	Ser	Leu	His	Tyr	Leu	Phe	Met	Gly	Ala	Ser
1				5					10					15	
Glu	Gln	Asp	Leu	Gly	Leu	Ser	Leu	Phe	Glu	Ala	Leu	Gly	Tyr	Val	Asp
		20						25					30		
Asp	Gln	Leu	Phe	Val	Phe	Tyr	Asp	Asp	Glu	Ser	Arg	Arg	Val	Glu	Pro
		35					40					45			
Arg	Thr	Pro	Trp	Val	Ser	Ser	Arg	Ile	Ser	Ser	Gln	Met	Trp	Leu	Gln
	50					55					60				
Leu	Ser	Gln	Ser	Leu	Lys	Gly	Trp	Asp	His	Met	Phe	Thr	Val	Asp	Phe
65					70					75				80	
Trp	Thr	Ile	Met	Glu	Asn	His	Asn	His	Ser	Lys	Glu	Ser	His	Thr	Leu
			85						90				95		
Gln	Val	Ile	Leu	Gly	Cys	Glu	Met	Gln	Glu	Asp	Asn	Ser	Thr	Glu	Gly
			100					105					110		
Tyr	Trp	Lys	Tyr	Gly	Tyr	Asp	Gly	Gln	Asp	His	Leu	Glu	Phe	Cys	Pro
		115					120						125		
Asp	Thr	Leu	Asp	Trp	Arg	Ala	Ala	Glu	Pro	Arg	Ala	Trp	Pro	Thr	Lys
	130					135					140				
Leu	Glu	Trp	Glu	Arg	His	Lys	Ile	Arg	Ala	Arg	Gln	Asn	Arg	Ala	Tyr
145					150					155					160
Leu	Glu	Arg	Asp	Cys	Pro	Ala	Gln	Leu	Gln	Gln	Leu	Leu	Glu	Leu	Gly

Arg	Gly	Val	Leu	165	Gln	Gln	Val	Pro	170	Leu	Val	Lys	Val	175	Thr	His
			180	Asp				185					190			
His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr	
		195					200					205				
Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met	
	210					215					220					
Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	Gly	Asp	Gly	
225					230					235					240	
Thr	Tyr	Gln	Gly	Trp	Ile	Thr	Leu	Ala	Val	Pro	Pro	Gly	Glu	Glu	Gln	
				245					250					255		
Arg	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Gly	Leu	Asp	Gln	Pro	Leu	Ile	
			260					265					270			
Val	Ile	Trp	Glu													
		275														

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg	Leu	Leu	Arg	Ser	His	Ser	Leu	His	Tyr	Leu	Phe	Met	Gly	Ala	Ser
1				5					10					15	
Glu	Gln	Asp	Leu	Gly	Leu	Ser	Leu	Phe	Glu	Ala	Leu	Gly	Tyr	Val	Asp
			20					25					30		
Asp	Gln	Leu	Phe	Val	Phe	Tyr	Asp	His	Glu	Ser	Arg	Arg	Val	Glu	Pro
		35					40					45			
Arg	Thr	Pro	Trp	Val	Ser	Ser	Arg	Ile	Ser	Ser	Gln	Met	Trp	Leu	Gln
		50				55					60				
Leu	Ser	Gln	Ser	Leu	Lys	Gly	Trp	Asp	His	Met	Phe	Thr	Val	Asp	Phe
65					70					75					80
Trp	Thr	Ile	Met	Glu	Asn	His	Asn	Ala	Ser	Lys	Glu	Ser	His	Thr	Leu
			85					90						95	
Gln	Val	Ile	Leu	Gly	Cys	Glu	Met	Gln	Glu	Asp	Asn	Ser	Thr	Glu	Gly
			100					105					110		
Tyr	Trp	Lys	Tyr	Gly	Tyr	Asp	Gly	Gln	Asp	Ala	Leu	Glu	Phe	Cys	Pro
		115					120					125			
Asp	Thr	Leu	Asp	Trp	Arg	Ala	Ala	Glu	Pro	Arg	Ala	Trp	Pro	Thr	Lys
		130				135					140				
Leu	Glu	Trp	Glu	Arg	His	Lys	Ile	Arg	Ala	Arg	Gln	Asn	Arg	Ala	Tyr
145					150					155					160
Leu	Glu	Arg	Asp	Cys	Pro	Ala	Gln	Leu	Gln	Gln	Leu	Leu	Glu	Leu	Gly
				165				170						175	
Arg	Gly	Val	Leu	Asp	Gln	Gln	Val	Pro	Pro	Leu	Val	Lys	Val	Thr	His
			180					185					190		
His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr
		195					200					205			
Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met
	210					215					220				
Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	Gly	Asp	Gly
225					230					235					240
Thr	Tyr	Gln	Gly	Trp	Ile	Thr	Leu	Ala	Val	Pro	Pro	Gly	Glu	Glu	Gln
				245					250					255	
Arg	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Gly	Leu	Asp	Gln	Pro	Leu	Ile
			260					265					270		
Val	Ile	Trp	Glu												
		275													

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg  
1 5 10

294960-104960